

WO 00/28057

PCT/US99/26478

SEQUENCE LISTING

&lt;110&gt; E. I. du Pont de Nemours and Company

&lt;120&gt; Plant Aminoacyl-tRNA Synthetases

&lt;130&gt; BB1270

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 60/107,789

&lt;151&gt; 1998-November-10

&lt;160&gt; 22

&lt;170&gt; Microsoft Office 97

&lt;210&gt; 1

&lt;211&gt; 1178

&lt;212&gt; DNA

&lt;213&gt; Zea mays

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&lt;210&gt; 2

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Zea mays

&lt;400&gt; 2

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Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
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His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
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Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
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Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Pro  
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Ser Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val  
100 105 110

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Arg Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu  
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Tyr Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe  
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Glu Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr  
195 200 205

Ala His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val  
210 215 220

Glu Glu Leu Lys Met Ser Gly Ala Ile Ser Leu Asp His Pro Asp Glu  
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Arg Val Leu Gly Leu Tyr Leu Ile Arg Phe Ala Glu Val Val Glu Glu  
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Ala Cys Thr Asn Leu Leu Pro Asn Val Val Cys Glu Tyr Leu Tyr Asn  
260 265 270

Leu Ser Glu Met Phe Thr Lys Phe Tyr Thr Asn Cys Gln Val Val Gly  
275 280 285

Ser Pro Glu Glu Thr Ser Arg Leu Leu Leu Cys Gln Ala Thr Ala Val  
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Val Met Arg Gln Cys Phe Asn Leu Leu Gly Ile Thr Pro Val Tyr Lys  
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<211> 2019  
<212> DNA  
<213> Oryza sativa

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<211> 587  
<212> PRT  
<213> Oryza sativa

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Glu Val Ser Lys Pro Gly Phe Gly Asp Tyr Gln Cys Asn Asn Ala Met  
35 40 45  
Ser Val Phe Ser Arg Ile Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro  
50 55 60  
Met Ala Val Gly Gln Ala Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile  
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Ile Glu Ser Ile Ser Val Ala Gly Pro Gly Tyr Ile Asn Ile Thr Leu  
85 90 95

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Ser Ser Asn Trp Ile Ala Gln Arg Ile Gln Asp Met Leu Val Cys Gly  
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 Ile Lys Thr Trp Ala Pro Ile Leu Pro Val Lys Arg Ala Val Leu Asp  
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 Phe Ser Ser Pro Asn Ile Ala Lys Glu Met His Val Gly His Ile Arg  
 130 135 140  
 Ser Thr Ile Ile Gly Asp Thr Leu Ala His Met Phe Glu Phe Thr Asn  
 145 150 155 160  
 Val Glu Val Leu Arg Arg Asn His Val Gly Asp Trp Gly Thr Gln Phe  
 165 170 175  
 Gly Met Leu Ile Glu Phe Leu Phe Glu Gln Phe Pro Asp Trp Glu Asp  
 180 185 190  
 Val Gly Asn Gln Ala Val Gly Asp Leu Gln Ser Phe Tyr Lys Ala Ser  
 195 200 205  
 Lys Lys Arg Phe Asp Asp Asp Pro Asp Phe Lys Glu Arg Ala Arg Gln  
 210 215 220  
 Ala Val Val Arg Leu Gln Gly Gly Glu Asp Lys Tyr Arg Ala Ala Trp  
 225 230 235 240  
 Lys Lys Ile Cys Gln Ile Ser Arg Met Glu Phe Asp Leu Val Tyr Lys  
 245 250 255  
 Arg Leu Asn Val Lys Leu Glu Glu Lys Gly Glu Ser Phe Tyr Asn Pro  
 260 265 270  
 Tyr Ile Pro Pro Val Leu Glu Glu Leu Thr Asn Lys Gly Leu Ile Val  
 275 280 285  
 Glu Ser Lys Gly Ala Arg Val Ile Phe Val Glu Asp His Pro Leu Ile  
 290 295 300  
 Val Ile Lys Gln Asp Gly Gly Phe Asn Tyr Ala Ser Thr Asp Leu Ala  
 305 310 315 320  
 Ala Leu Trp Tyr Arg Leu Asn Val Glu Lys Ala Glu Trp Ile Ile Tyr  
 325 330 335  
 Val Thr Asp Val Gly Gln Gln Arg His Phe His Met Leu Phe Thr Ala  
 340 345 350  
 Ala Lys Met Ala Gly Trp Leu Pro Glu Gln Asn Gly Lys Lys Tyr Pro  
 355 360 365  
 Lys Ala Ser His Val Gly Phe Gly Leu Val Leu Gly Ser Asp Gly Lys  
 370 375 380  
 Arg Phe Arg Thr Arg Cys Ser Glu Val Val Arg Leu Val Asp Leu Leu  
 385 390 395 400  
 Asp Glu Ala Lys Ala Arg Ser Lys Ala Gln Leu Ile Lys Arg Phe Thr  
 405 410 415

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 Ser Glu Ala Ile Gly Tyr Gly Ala Val Lys Tyr Ser Asp Leu Lys Asn  
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 Asn Arg Leu Thr Asp Tyr Thr Phe Ser Phe Asp Gln Met Leu Ser Asp  
 450 455 460  
 Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile Cys  
 465 470 475 480  
 Ser Ile Ile Arg Lys Ala Ser Lys Asp Val Glu Lys Leu Lys Met Thr  
 485 490 495  
 Gly Ala Ile Thr Leu Gly His Pro Tyr Glu Arg Phe Leu Gly Leu His  
 500 505 510  
 Leu Ile Gln Phe Thr Glu Val Val Glu Gln Ala Cys Ala Asp Leu Gln  
 515 520 525  
 Pro His Arg Leu Cys Asp Tyr Leu Tyr Ser Leu Ser Leu Thr Phe Ser  
 530 535 540  
 Lys Phe Tyr Thr Asn Cys Gln Val Val Gly Ser Pro Glu Glu Thr Ser  
 545 550 555 560  
 Arg Leu Leu Leu Cys Glu Ala Thr Gly Ile Ile Met Arg Gln Cys Phe  
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 <212> DNA  
 <213> Glycine max

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 <211> 288  
 <212> PRT  
 <213> Glycine max

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 Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
 35 40 45  
 Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
 50 55 60  
 Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
 65 70 75 80  
 Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Ser Ser Glu  
 85 90 95  
 Val Val Arg Leu Val Asp Leu Leu Asp Glu Ala Lys Arg Arg Cys Lys  
 100 105 110  
 Ile Ala Ile Leu Glu Arg Asp Thr Thr Lys Asp Trp Ser Glu Glu Glu  
 115 120 125  
 Ile Glu Lys Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala  
 130 135 140  
 Asp Leu Lys Ile Asn Arg Leu Thr Asn Tyr Thr Phe Asn Phe Asp Gln  
 145 150 155 160  
 Met Leu Asn Asp Lys Gly Asn Thr Ala Val Tyr Leu Leu Tyr Ala His  
 165 170 175  
 Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Gly Lys Asp Ile Glu Glu  
 180 185 190  
 Val Lys Arg Asn Gly Lys Ile Val Leu Asp His Glu Asp Glu Arg Ala  
 195 200 205  
 Leu Gly Leu His Leu Leu Gln Phe Pro Glu Val Phe Glu Glu Ala Cys  
 210 215 220  
 Thr Asn Leu Leu Pro Asn Phe Leu Cys Glu Tyr Leu Tyr Asn Leu Ala  
 225 230 235 240  
 Glu Ile Phe Thr Lys Lys Phe Tyr Ala Asn Cys Gln Val Val Gly Ser  
 245 250 255  
 Pro Glu Glu Thr Ser Arg Leu Leu Leu Cys Glu Ala Thr Val Thr Val  
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 <212> DNA  
 <213> Triticum aestivum

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 <212> PRT  
 <213> Triticum aestivum

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 Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu  
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 Glu Leu Glu Gln Thr Ser Lys Ala Val Gly Tyr Gly Ala Val Lys Tyr  
 85 90 95  
 Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Asp  
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 115 120 125  
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 Glu Leu Lys Val Ser Gly Asn Ile Ser Leu Ala His Pro Asp Glu Arg  
 145 150 155 160

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Val Leu Gly Leu Tyr Leu Ile Arg Tyr Ala Glu Ile Val Glu Glu Ala  
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Cys Thr Asn Leu Leu Pro Ser Val Leu Cys Glu Tyr Leu Tyr Asn Leu  
 180 185 190

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 <212> DNA  
 <213> Zea mays

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tattgttgca ttgtacactt taatattgta ctgtgattag gctttactcg cggtggatgt 2460
ctttcaccgc tagatggcca gaggcataatc ctgccaaacca agcagagcag ccattttgat 2520
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<210> 10  
 <211> 715  
 <212> PRT  
 <213> Zeb mays

<400> 10  
 Met Glu Ala Ala Leu Ser Phe Ser Lys Asp Ser Pro Pro Ile Ser Ile  
 1 5 10 15  
 Ile Cys Ala Ala Lys Leu Val Gly Leu Pro Leu Thr Ile Asn His Ser  
 20 25 30  
 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser  
 35 40 45  
 Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser  
 50 55 60  
 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val  
 65 70 75 80  
 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu  
 85 90 95  
 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu  
 100 105 110  
 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu  
 115 120 125  
 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr  
 130 135 140  
 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu  
 145 150 155 160  
 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly  
 165 170 175  
 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp  
 180 185 190  
 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val  
 195 200 205  
 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His  
 210 215 220  
 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly  
 225 230 235 240  
 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn  
 245 250 255

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Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys  
 260 265 270  
 Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu  
 275 280 285  
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr  
 290 295 300  
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg  
 305 310 315 320  
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met  
 325 330 335  
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu  
 340 345 350  
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg  
 355 360 365  
 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr  
 370 375 380  
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val  
 385 390 395 400  
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr  
 405 410 415  
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu  
 420 425 430  
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu  
 435 440 445  
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg  
 450 455 460  
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala  
 465 470 475 480  
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu  
 485 490 495  
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro  
 500 505 510  
 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe  
 515 520 525  
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg  
 530 535 540  
 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn  
 545 550 555 560  
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Asn Lys Gly Glu  
 565 570 575

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Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys  
580 585 590

Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu  
595 600 605

Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile  
610 615 620

Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser  
625 630 635 640

Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro  
645 650 655

Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn  
660 665 670

Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg  
675 680 685

Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala  
690 695 700

Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser  
705 710 715

<210> 11  
<211> 1920  
<212> DNA  
<213> Oryza sativa

<220>  
<221> unsure  
<222> (139)

<220>  
<221> unsure  
<222> (238)

<220>  
<221> unsure  
<222> (431)

<400> 11  
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cccgagggtg ccgccgcgcc tcctgcggcc ccacctccgc cggccctctc cgtccgcgcc 120  
tccgcctccg cctcggcgnc accggacggc gccggcggcc cgggtcgggc ccgttcgcgc 180  
cgtcgccgac ggcaacctcc acgtcggcgg cgcccgacc gcgcacttca actacctntt 240  
cgcgcggtcc aaggggggca agttcgtgct ccgcatcgag gacaccgact tcgagaggtc 300  
caccaagaag tccgaggagg ccgtgctcag tgacctcgcc tggctcggcc ttgactggga 360  
cgaaggcccg gatgtcgggtg gggaatatgg gcccgatcgc cagtccgagc gcaattcgat 420  
gtacaaacag natgccgaga agctgatgga gtctggggca gtctatcagt gcttttactc 480  
cagtgaggga cttgaacaga tgaaggaaac tgcaagcaga tgcaaccttc cacctgtata 540  
cattggcaag tgggggactg cttcagatgc agaaatacaa caggagttag agaaggggac 600  
accttacact taccgtttcc gtgtaccgaa ggaagggtcg ttgaaaatta atgaccttat 660  
tcgtggtgag gtcagttgga acttagacac gcttggtgat ttcgtgatta tgagaagcaa 720  
tggccagcca gtgtataact tctgtgtcac agttgatgat gctaccatgc gcatctctca 780  
tgttatcaga gctgaagaac atctgcaaaa cacattacgg caggctctta ttataaagc 840  
acttgattt ccaatgcctt cgtttgctca tgtatcactt attctagctc ctgatagaag 900

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taaactgtct aaacgtcatg gggctacttc tgtgggacag tacaaagaga tgggctattt 960
gcctcaggca atggtaaatt atttggcact tcttgggttg ggtgatggta ctgaaaatga 1020
gttcttcacc attgatgacc tagtggaaaa attcactata aatcgtgtca acaaaagtgg 1080
agcagtcctt gatgctgtaa aattaaaatg gatgaatgga caacatctaa gatcatttcc 1140
ccctgatgta ctcatcaaga gttttgagga tagatggaag gacacaggca ttctccagga 1200
gtctgaaagt ggttttgcta aagaagcggc tgagcttttg aaggatggca tcgatttgat 1260
cactgatgct gacgcagccc tttcaaacct gttgtcgtat cccctccatg ctacattaag 1320
cagtgatgaa gctaaatctg tgggtgcaaga caagctttct gaggttgcac caggactcat 1380
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gctccgtgta ctgctgactg gcaagcttca tgggcctgac atgggcggca ccgtagtcc 1560
catacacaaa gccggcacct gtggagcggc cactcagcaa tccggtttcg taaatctcga 1620
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gagtttttgt tttctgtaat actccactat aaagcatagg atatgttcca ttttactacc 1800
catttctaca gttgtgagga aactatagtt tccggtttct gtagttaata aagcggaatt 1860
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<210> 12  
 <211> 555  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> UNSURE  
 <222> (130)

<400> 12  
 Leu Arg Ile Arg Leu Leu Pro Glu Val Pro Pro Arg Leu Leu Arg Pro  
 1 5 10 15  
 His Leu Arg Arg Pro Ser Pro Ser Ala Pro Pro Pro Pro Arg Arg  
 20 25 30  
 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala  
 35 40 45  
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr  
 50 55 60  
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp  
 65 70 75 80  
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser  
 85 90 95  
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly  
 100 105 110  
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys  
 115 120 125  
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe  
 130 135 140  
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys  
 145 150 155 160  
 Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala  
 165 170 175

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Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe  
 180 185 190  
 Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly  
 195 200 205  
 Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg  
 210 215 220  
 Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala  
 225 230 235 240  
 Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn  
 245 250 255  
 Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro  
 260 265 270  
 Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu  
 275 280 285  
 Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly  
 290 295 300  
 Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly  
 305 310 315 320  
 Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys  
 325 330 335  
 Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val  
 340 345 350  
 Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp  
 355 360 365  
 Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu  
 370 375 380  
 Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys  
 385 390 395 400  
 Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu Ser Asn Leu  
 405 410 415  
 Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser  
 420 425 430  
 Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala  
 435 440 445  
 Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly  
 450 455 460  
 Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly  
 465 470 475 480  
 Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His  
 485 490 495

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PCT/US99/26478

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr  
500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg  
515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln  
530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser  
545 550 555

<210> 13  
<211> 731  
<212> DNA  
<213> Glycine max

<400> 13  
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agttcctccc attttccacc actctcacac ccttcgcacc ttcttcttcc aacgacgccg 120  
ttttctcaagt ctctgctctc tccgaacaac caccaccggt tcgcttctgt ttcgctcctt 180  
ctcccaccgg aaacctccac gtggcggtg cccgaacggc cctcttcaac tacttggtcg 240  
caaggtccaa aggtgggaaa tttgtgctga gaattgagga cactgacttg gagaggtcca 300  
caaggaggatc tgaggaggcc atgctcaaag atctttcttg gcttggactt gattgggatg 360  
aagggcctgg tggtggaggg gattatggtc cttataggca gtctgatagg aattctttat 420  
acaagcaatt tgcggataac ctacaccaat ccggtcatgt ttatcgctgc ttctgttcta 480  
atgaggaact agagaaaatg aaggaggatg ctaaaactaaa gcaactgcct ccagtgtaca 540  
caggtaaatg ggccagtgc acaaatgagg aagtagaaga agagctagca aaaggaactc 600  
cttacctta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660  
gcgaagttag ttggaacttg gatacgcttg gagattttgt gataatgagg agtaatggtc 720  
agcctgttta t 731

<210> 14  
<211> 404  
<212> PRT  
<213> Glycine max

<400> 14  
Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
1 5 10 15  
Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
20 25 30  
Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr  
35 40 45  
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
50 55 60  
Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg  
65 70 75 80  
Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His  
85 90 95  
Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu  
100 105 110

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Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr  
 115 120 125  
 Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala  
 130 135 140  
 Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu  
 145 150 155 160  
 Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr  
 165 170 175  
 Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn  
 180 185 190  
 Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile  
 195 200 205  
 Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr  
 210 215 220  
 Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile  
 225 230 235 240  
 Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser  
 245 250 255  
 Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn  
 260 265 270  
 Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe  
 275 280 285  
 Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys  
 290 295 300  
 Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln  
 305 310 315 320  
 His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu  
 325 330 335  
 Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile  
 340 345 350  
 Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp  
 355 360 365  
 Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr  
 370 375 380  
 Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu  
 385 390 395 400  
 Val Ala Lys Ser

<210> 15  
 <211> 407

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<212> DNA  
 <213> Triticum aestivum

<220>  
 <221> unsure  
 <222> (14)

<220>  
 <221> unsure  
 <222> (150)

<220>  
 <221> unsure  
 <222> (293)

<220>  
 <221> unsure  
 <222> (341)

<220>  
 <221> unsure  
 <222> (350) .. (351)

<220>  
 <221> unsure  
 <222> (383)

<220>  
 <221> unsure  
 <222> (399)

<220>  
 <221> unsure  
 <222> (401)

<400> 15  
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 ttcagcactc tttgttcccg tcgtacaaaa tttcaaaatt ctctcagtga gcgattgcct 120  
 gcaaggacgc gattcgcgcc gtcaccaaca gggaatcttc atcttggttc cctacgtacg 180  
 gccctcttca attacctgat tgcaaaagct acacgcggtg aattcatcct acgcatagag 240  
 gacacagatn agtcaaggac tggtcctggg gcgattgaaa aactctgcgc tgnnttgaga 300  
 tggggggggt taaaaaggga taaaagggct ggtccccaat ngaccgcaan ngggcctttc 360  
 aaaaatctca aaagactttt aangttataa aaaaaaacnc nccataa 407

<210> 16  
 <211> 79  
 <212> PRT  
 <213> Triticum aestivum

<220>  
 <221> UNSURE  
 <222> (55)

<220>  
 <221> UNSURE  
 <222> (69)

<400> 16  
 Lys Phe Gln Asn Ser Leu Ser Glu Arg Leu Pro Ala Arg Thr Arg Phe  
 1 5 10 15





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<210> 18  
 <211> 495  
 <212> PRT  
 <213> Zea mays

<400> 18

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Met Leu Leu Arg Asp His Val Thr Asn Gly Ser Thr Val Ala Ala Met
 1          5          10          15

Asn Ser Ala Ser Val Ala Glu Trp Ala Thr Ser Leu Ser Leu Leu Phe
          20          25          30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
          35          40          45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
 50          55          60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
 65          70          75          80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
          85          90          95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
          100          105          110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Gly Glu Leu Cys
          115          120          125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
          130          135          140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
          145          150          155          160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
          165          170          175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
          180          185          190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
          195          200          205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
          210          215          220

Cys Gly Val Pro Pro Gln Lys Phe Arg Thr Val Cys Ser Ser Ile Asp
          225          230          235          240

Lys Leu Asp Lys Gln Thr Phe Glu Gln Val Lys Lys Glu Leu Val Asp
          245          250          255

Glu Lys Gly Ile Ser Asn Glu Thr Ala Asp Glu Ile Gly Asn Leu Val
          260          265          270

Lys Thr Arg Gly Pro Pro Leu Glu Val Leu Met Glu Leu Arg Lys Glu
          275          280          285

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Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu  
 290 295 300  
 Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys  
 305 310 315 320  
 Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly  
 325 330 335  
 Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile  
 340 345 350  
 Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys  
 355 360 365  
 Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala  
 370 375 380  
 Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr  
 385 390 395 400  
 Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala  
 405 410 415  
 Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe  
 420 425 430  
 Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser  
 435 440 445  
 Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly  
 450 455 460  
 Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Glu Val Asp  
 465 470 475 480  
 Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser  
 485 490 495

<210> 19  
 <211> 754  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (18)

<220>  
 <221> unsure  
 <222> (610)

<220>  
 <221> unsure  
 <222> (713)

<220>  
 <221> unsure  
 <222> (720)

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&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (740)

&lt;400&gt; 19

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ggaacatgga tattattngt gttcccgggg ttatggctga agcagagctt atagcttcta 60
tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aagggttcca 120
gtcgaaaagg tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
agtcattgac cgagtttagaa gagagacttg ggagcagtg ggaagcagtt gctgatctga 360
aacagctatt ctcccttgct gaaaaaattg gttactctaa atggcttcaa tttgatgcat 420
cagttgttcg aggtcttgct tactacactg gcattgtatt tgagggtttt gaccgagaag 480
gaaagctgcg agctatctgt ggtggtggc gatatgatca tttgttctca acttttggtg 540
ctgatgacat tgctgcatgt ggttttggat ttggtgatgc aagtcatagt ggaattgctc 600
aaaagagaan ggtctgttac cgggaaagctt aacttgcaaa tagatgacat tgtgtgtgcc 660
ttggaccaaa gatcttcaag ggatgtgctg ctatggggcc caacaatctc agngaaaaan 720
ggcaaattgt tgaagttggn tttgggaaaa caaa 754

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&lt;210&gt; 20

&lt;211&gt; 243

&lt;212&gt; PRT

&lt;213&gt; Glycine max

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (6)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (203)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (235)

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (238)

&lt;400&gt; 20

```

Asn Met Asp Ile Ile Xaa Val Pro Gly Val Met Ala Glu Ala Glu Leu
 1           5           10           15

```

```

Ile Ala Ser Ile Val Thr Leu Phe Lys Arg Ile Gly Ile Thr Glu Ser
      20           25           30

```

```

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
      35           40           45

```

```

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
      50           55           60

```

```

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
      65           70           75           80

```

```

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
      85           90           95

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Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser  
 100 105 110  
 Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys  
 115 120 125  
 Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly  
 130 135 140  
 Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly  
 145 150 155 160  
 Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser  
 165 170 175  
 Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp  
 180 185 190  
 Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu  
 195 200 205  
 Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys  
 210 215 220  
 Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile  
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 Val Glu Val

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 <212> DNA  
 <213> Triticum aestivum

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 tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180  
 gtcattctgaa gcagtacagg gcatcattga agtgctctct ctcaagtcac tgtccaaact 240  
 tgaagaggtg ctaggctcag gtgttgaagc cgttgctgac ttgaagaagc tcttctcgct 300  
 tgctgagcaa tatggttatt ctgattggat ctgtttcgat gcatctgttg ttcgtggcct 360  
 tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat 420  
 ttgtgggtggg gggaggtatg acaggctact gtcaacattt ggaactgaag atgtaccagc 480  
 ctgtggcctt ggatttggag atgctgtcat agtggagctg ctgaaagaaa agggtctttt 540  
 gcctgacctg ccacgtcaaa tagatgacat tgtgttccca ttggacgagg agcttgaggg 600  
 gccagcatct agtggttgcatt cctgtctgag gaagaagggc agatctgtag acctttaga 660  
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 cttgggttggg aaatccgagt gggagcgagg catggtccgt gtgaagatac tatcaaccag 780  
 agaagagttc gaggtcaagg cgggcgaatt gcagtagctg ttagctgacg tggtcgattt 840  
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 ttcacgtcgt gtatacaaac aattaggtgg ctttgaatgc tattgccatc ttctttcgga 960  
 tcattcacct tgcaacaaac aaagaaattg taggttttgc cattcaccaa catgtattga 1020  
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<210> 22  
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&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 22

Lys Leu Gly Ile Thr Ser Ser Asp Val Gly Ile Arg Leu Ser Ser Arg  
 1 5 10 15

Lys Val Leu Gln Ala Val Leu Asp Met Tyr Ser Val Pro Gln His Leu  
 20 25 30

Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg  
 35 40 45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala  
 50 55 60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu  
 65 70 75 80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys  
 85 90 95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe  
 100 105 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe  
 115 120 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly Gly  
 130 135 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala  
 145 150 155 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu  
 165 170 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe  
 180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys  
 195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu  
 210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile  
 225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile  
 245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln  
 260 265 270

&lt;210&gt; 23

&lt;211&gt; 913

&lt;212&gt; DNA

&lt;213&gt; Zea mays

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 ttaagagtga tgggtggcttc aactatgcct caacagactt aactgctctt tggatcggc 180  
 tcaatggtga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240  
 ttgacatggt ttccagtgcg gcaaagatgg ccggttggct ccagatcca agtgaaaaga 300  
 agtttccgaa aacaagccat gttggatttg gtcttggtct tggttcaaga tggcaagcgg 360  
 ttccgaaccc gcagtactga ggttggttca ttggttagagc tacttgatga ggctaaatct 420  
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480  
 gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540  
 ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600  
 ggaaataactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tattcggaaa 660  
 tccaacaaga acgtggnaga ctgaagagat ggagccattt ctctcgacca tccggattag 720  
 cgctgttggg gctgtatctt anccgatttg cagagttggt gaagaggatc acgaactact 780  
 ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840  
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 ctcggatacn cat 913

<210> 24  
 <211> 221  
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 His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr  
 35 40 45  
 Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln  
 50 55 60  
 Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
 65 70 75 80  
 Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa  
 85 90 95  
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu  
 100 105 110  
 Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 115 120 125  
 Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu  
 130 135 140  
 Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln  
 145 150 155 160  
 Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys  
 165 170 175  
 Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser  
 180 185 190  
 Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile  
 195 200 205  
 Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp  
 210 215 220

<210> 25  
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 <212> DNA  
 <213> Oryza sp.



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 ggttttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc 180  
 gcaacaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240  
 tcaaatatta tcgaatccat ctctgttgcc gganctgggt acattaacat aacggttatcc 300  
 agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360  
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420  
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa 480  
 ctcaaaangg ttgnggntca caaaanggtt aanttctcn acgtaaacan gttgggaaac 540  
 nggggnacac a 551

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 <212> PRT  
 <213> Oryza sp.

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 20 25 30  
 Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val  
 35 40 45  
 Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala  
 50 55 60  
 Gln Arg Ile Gln  
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<210> 27  
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 acaactgac tagcatcact ttggtatcgt ctaaatgaag aaaaacttga atggattgta 120  
 tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180  
 gcaggttggt taccaaagga tgagaatgct tatccaaaat gtactcatat aggttttggt 240  
 cttgttcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300  
 gttgattact tgatgaagct aaaangcgct gtaaaattgc cntcttgaaa cgtgatacaa 360  
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<210> 28  
 <211> 115  
 <212> PRT  
 <213> Glycine max

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 <222> (96)

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 Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly  
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 Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn  
             20                    25                    30  
 Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
             35                    40                    45  
 Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
             50                    55                    60  
 Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
             65                    70                    75                    80  
 Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa  
                     85                    90                    95  
 Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys  
                     100                    105                    110  
 Leu Pro Ser  
             115

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<212> DNA  
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 ctctgtagtac tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180  
 aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240  
 gaaggaaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300  
 tctgaaagaa taaccgactg actaattaca ctccaacttt gattcaagan ctaagtgaca 360  
 agggaataac tgctgtcnac ttcaataagc caagcccgta cctccancca ttcnaaaacc 420  
 caacatggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480  
 gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540  
 aaactatnac taccnaagta aaagt 565

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 <211> 33  
 <212> PRT  
 <213> Triticum sp.

<400> 30  
 Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
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 Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 20 25 30

Leu

<210> 31  
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 <212> DNA  
 <213> Oryza sp.

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 catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgctgt atccctcca 180

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tgctacatta agcagtgatg aagctaaatc tgtggtgcaa gacaagcttt ctgaggttgc 240
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tgatggttgg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360
actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420
caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcactcaaca atccggtttc 480
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 <213> Oryza sp.

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 Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu  
 20 25 30  
 Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu  
 35 40 45  
 Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu  
 50 55 60  
 Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu  
 65 70 75 80  
 Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly  
 85 90 95  
 Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys  
 100 105 110  
 Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly  
 115 120 125  
 Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys  
 130 135 140  
 Ala Gly Thr  
 145

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 tctccgaaca accaccacc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180  
 acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaaggtcc aaaggtggga 240  
 aatttgtgct gagaattgag gacactgact tggagaggtc caagtaggga gtctgaggag 300  
 gccatgctca aagatctttc ttggcttgga cttgattggg atgaagggcc tgggtgttg 360  
 aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420  
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<210> 34  
 <211> 94  
 <212> PRT  
 <213> Glycine max

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 <221> UNSURE  
 <222> (63)

<400> 34  
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 Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
 20 25 30  
 Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
 35 40 45  
 Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser  
 50 55 60  
 Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
 65 70 75 80  
 Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro  
 85 90

<210> 35  
 <211> 506  
 <212> DNA  
 <213> Glycine max

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 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180  
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
 tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
 agtcattgac cgagtttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360  
 acagtattct cccttgctga aaaaattggg tactctaaat ggttcaattt gatgatagtt 420  
 gttcgaggctc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480  
 gcntctgtgt gtgtcaatac attgnn 506

<210> 36  
 <211> 48  
 <212> PRT  
 <213> Glycine max

<400> 36  
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 1 5 10 15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 20 25 30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 35 40 45

<210> 37  
 <211> 577  
 <212> DNA  
 <213> Triticum sp.

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Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile  
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